IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Reissue Application of:

CRAIG A. SMITH et al

Appln. No.: **09/144,502**   Group Art Unit: **1646**

Filed: **August 31, 1998**   Examiner: **Fitzgerald, D.**

Reissue of: **U.S. Patent 5,712,155**

Issued: **January 27, 1998**

For: **DNA ENCODING TUMOR NECROSIS FACTOR-α AND -β RECEPTORS**

PROPOSED DRAWING CORRECTIONS

Assistant Commissioner
    for Patents
Washington, D.C. 20231

Sir:

In response to the teleconference on May 27, 1999, wherein the Examiner requested that Applicants provide proposed drawings corrections, Applicants submit herewith 5 sheets of proposed drawing corrections, wherein it is proposed that Figures 2A-2B and 3A-3C be deleted in their entirety (see the Preliminary Amendment filed October 9, 1998, wherein Figures 2A-2B and 3A-3C were deleted and replaced by the Sequence Listing).

Applicants respectfully request that the Examiner approve the proposed corrections.

The Examiner is invited to contact the undersigned at his Washington telephone number on any questions which might arise.

Respectfully submitted,

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Dated: May 28, 1999

Figure 2A

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                                       GCGAGGCAGGCAGCCTGGAGAGAAGGCG           29

CTGGGCTGCGAGGGCGCGAGGGCGCGAGGGCAGGGGGCAACCGGACCCCGCCCGCATCC                 87

ATG GCG CCC GTC GCC GTC TGG GCC GCG CTG GCC GTC GGA CTG GAG                  132
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu                   -8

CTC TGG GCT GCG GCG CAC GCC TTG CCC GCC CAG GTG GCA TTT ACA                  177
Leu Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr                    8

CCC TAC GCC CCG GAG CCC GGG AGC ACA TGC CGG CTC AGA GAA TAC                  222
Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr                   23

TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA TGC TCG CCG GGC                  267
Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly                   38

CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC ACC GTG TGT                  312
Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys                   53

GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC TGG GTT                  357
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val                   68

CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT GAC CAG GTG                  402
Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val                   83

GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC ACC TGC                  447
Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys                   98

AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC CGG                  492
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg                  113

CTG TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC                  537
Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala                  128

AGA CCA GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC TGT GCC                  582
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala                  143

CCG GGG ACG TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC AGG                  627
Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg                  158

CCC CAC CAG ATC TGT AAC GTG GTG GCC ATC CCT GGG AAT GCA AGC                  672
Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser                  173

ATG GAT GCA GTC TGC ACG TCC ACG TCC CCC ACC CGG AGT ATG GCC                  717
Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala                  188

CCA GGG GCA GTA CAC TTA CCC CAG CCA GTG TCC ACA CGA TCC CAA                  762
Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln                  203

CAC ACG CAG CCA ACT CCA GAA CCC AGC ACT GCT CCA AGC ACC TCC                  807
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser                  218

TTC CTG CTC CCA ATG GGC CCC AGC CCC CCA GCT GAA GGG AGC ACT                  852
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr                  233

GGC GAC TTC GCT CTT CCA GTT GGA CTG ATT GTG GGT GTG ACA GCC                  897
Gly Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala                  248

TTG GGT CTA CTA ATA ATA GGA GTG GTG AAC TGT GTC ATC ATG ACC                  942
Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr                  263
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Figure 2B

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CAG GTG AAA AAG AAG CCC TTG TGC CTG CAG AGA GAA GCC AAG GTG        987
Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val        278

CCT CAC TTG CCT GCC GAT AAG GCC CGG GGT ACA CAG GGC CCC GAG       1032
Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu        293

CAG CAG CAC CTG CTG ATC ACA GCG CCG AGC TCC AGC AGC AGC TCC       1077
Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser        308

CTG GAG AGC TCG GCC AGT GCG TTG GAC AGA AGG GCG CCC ACT CGG       1122
Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg        323

AAC CAG CCA CAG GCA CCA GGC GTG GAG GCC AGT GGG GCC GGG GAG       1167
Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu        338

GCC CGG GCC AGC ACC GGG AGC TCA GAT TCT TCC CCT GGT GGC CAT       1212
Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His        353

GGG ACC CAG GTC AAT GTC ACC TGC ATC GTG AAC GTC TGT AGC AGC       1257
Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser        368

TCT GAC CAC AGC TCA CAG TGC TCC TCC CAA GCC AGC TCC ACA ATG       1302
Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met        383

GGA GAC ACA GAT TCC AGC CCC TCG GAG TCC CCG AAG GAC GAG CAG       1347
Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln        398

GTC CCC TTC TCC AAG GAG GAA TGT GCC TTT CGG TCA CAG CTG GAG       1392
Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu        413

ACG CCA GAG ACC CTG CTG GGG AGC ACC GAA GAG AAG CCC CTG CCC       1437
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro        428

CTT GGA GTG CCT GAT GCT GGG ATG AAG CCC AGT                       1470
Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser                        439

TAACCAGGCCGGTGTGGGCTGTGTCGTAGCCAAGGTGGGCTGAGCCCTGGCAGGATGAC

CCTGCGAAGGGGCCCTGGTCCTTCCAGGCCCCCACCACTAGGACTCTGAGGCTCTTTCT

GGGCCAAGTTCCTCTAGTGCCCTCCACAGCCGCAGCCTCCCTCTGACCTGCAG...
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Figure 3A

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                                    CGCAGCTGAGGCACTAGAGCTCC        23

AGGCACAAGGGCGGGAGCCACCGCTGCCCCT ATG GCG CCC GCC GCC CTC TGG    75
                                Met Ala Pro Ala Ala Leu Trp   -16

GTC GCG CTG GTC TTC GAA CTG CAG CTG TGG GCC ACC GGG CAC ACA   120
Val Ala Leu Val Phe Glu Leu Gln Leu Trp Ala Thr Gly His Thr    -1

GTG CCC GCC CAG GTT GTC TTG ACA CCC TAC AAA CCG GAA CCT GGG   165
Val Pro Ala Gln Val Val Leu Thr Pro Tyr Lys Pro Glu Pro Gly    15

TAC GAG TGC CAG ATC TCA CAG GAA TAC TAT GAC AGG AAG GCT CAG   210
Tyr Glu Cys Gln Ile Ser Gln Glu Tyr Tyr Asp Arg Lys Ala Gln    30

ATG TGC TGT GCT AAG TGT CCT CCT GGC CAA TAT GTG AAA CAT TTC   255
Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val Lys His Phe    45

TGC AAC AAG ACC TCG GAC ACC GTG TGT GCG GAC TGT GAG GCA AGC   300
Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu Ala Ser    60

ATG TAT ACC CAG GTC TGG AAC CAG TTT CGT ACA TGT TTG AGC TGC   345
Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser Cys    75

AGT TCT TCC TGT ACC ACT GAC CAG GTG GAG ATC CGC GCC TGC ACT   390
Ser Ser Ser Cys Thr Thr Asp Gln Val Glu Ile Arg Ala Cys Thr    90

AAA CAG CAG AAC CGA GTG TGT GCT TGC GAA GCT GGC AGG TAC TgC   435
Lys Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys   105

GCC TTG AAA ACC CAT TCT GGC AGC TGT CGA CAG TGC ATG AGG CTG   480
Ala Leu Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu   120

AGC AAG TGC GGC CCT GGC TTC GGA GTG GCC AGT TCA AGA GCC CCA   525
Ser Lys Cys Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro   135

AAT GGA AAT GTG CTA TGC AAG GCC TGT GCC CCA GGG ACG TTC TCT   570
Asn Gly Asn Val Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser   150

GAC ACC ACA TCA TCC ACT GAT GTG TGC AGG CCC CAC CGC ATC TGT   615
Asp Thr Thr Ser Ser Thr Asp Val Cys Arg Pro His Arg Ile Cys   165

AGC ATC CTG GCT ATT CCC GGA AAT GCA AGC ACA GAT GCA GTC TGT   660
Ser Ile Leu Ala Ile Pro Gly Asn Ala Ser Thr Asp Ala Val Cys   180

GCG CCC GAG TCC CCA ACT CTA AGT GCC ATC CCA AGG ACA CTC TAC   705
Ala Pro Glu Ser Pro Thr Leu Ser Ala Ile Pro Arg Thr Leu Tyr   195

GTA TCT CAG CCA GAG CCC ACA AGA TCC CAA CCC CTG GAT CAA GAG   750
Val Ser Gln Pro Glu Pro Thr Arg Ser Gln Pro Leu Asp Gln Glu   210

CCA GGG CCC AGC CAA ACT CCA AGC ATC CTT ACA TCG TTG GGT TCA   795
Pro Gly Pro Ser Gln Thr Pro Ser Ile Leu Thr Ser Leu Gly Ser   225

ACC CCC ATT ATT GAA CAA AGT ACC AAG GGT GGC ATC TCT CTT CCA   840
Thr Pro Ile Ile Glu Gln Ser Thr Lys Gly Gly Ile Ser Leu Pro   240

ATT GGT CTG ATT GTT GGA GTG ACA TCA CTG GGT CTG CTG ATG TTA   885
Ile Gly Leu Ile Val Gly Val Thr Ser Leu Gly Leu Leu Met Leu   255
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Figure 3B

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GGA CTG GTG AAC TGC ATC ATC CTG GTG CAG AGG AAA AAG AAG CCC    930
Gly Leu Val Asn Cys Ile Ile Leu Val Gln Arg Lys Lys Lys Pro    270

TCC TGC CTA CAA AGA GAT GCC AAG GTG CCT CAT GTG CCT GAT GAG    975
Ser Cys Leu Gln Arg Asp Ala Lys Val Pro His Val Pro Asp Glu    285

AAA TCC CAG GAT GCA GTA GGC CTT GAG CAG CAG CAC CTG TTG ACC   1020
Lys Ser Gln Asp Ala Val Gly Leu Glu Gln Gln His Leu Leu Thr    300

AC  GCA CCC AGT TCC AGC AGC AGC TCC CTA GAG AGC TCA GCC AGC   1065
Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser    315

GCT GGG GAC CGA AGG GCG CCC CCT GGG GGC CAT CCC CAA GCA AGA   1110
Ala Gly Asp Arg Arg Ala Pro Pro Gly Gly His Pro Gln Ala Arg    330

GTC ATG GCG GAG GCC CAA GGG TTT CAG GAG GCC CGT GCC AGC TCC   1155
Val Met Ala Glu Ala Gln Gly Phe Gln Glu Ala Arg Ala Ser Ser    345

AGG ATT TCA GAT TCT TCC CAC GGA AGC CAC GGG ACC CAC GTC AAC   1200
Arg Ile Ser Asp Ser Ser His Gly Ser His Gly Thr His Val Asn    360

GTC ACC TGC ATC GTG AAC GTC TGT AGC AGC TCT GAC CAC AGT TCT   1245
Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser    375

CAG TGC TCT TCC CAA GCC AGC GCC ACA GTG GGA GAC CCA GAT GCC   1290
Gln Cys Ser Ser Gln Ala Ser Ala Thr Val Gly Asp Pro Asp Ala    390

AAG CCC TCA GCG TCC CCA AAG GAT GAG CAG GTC CCC TTC TCT CAG   1335
Lys Pro Ser Ala Ser Pro Lys Asp Glu Gln Val Pro Phe Ser Gln    405

GAG GAG TGT CCG TCT CAG TCC CCG TGT GAG ACT ACA GAG ACA CTG   1380
Glu Glu Cys Pro Ser Gln Ser Pro Cys Glu Thr Thr Glu Thr Leu    420

CAG AGC CAT GAG AAG CCC TTG CCC CTT GGT GTG CCG GAT ATG GGC   1425
Gln Ser His Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Met Gly    435

ATG AAG CCC AGC CAA GCT GGC TGG TTT GAT CAG ATT GCA GTC AAA   1470
Met Lys Pro Ser Gln Ala Gly Trp Phe Asp Gln Ile Ala Val Lys    450

                                                              1476
GTG GCC                                                         452
Val Ala
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TGACCCCTGACAGGGGTAACACCCTGCAAAGGGACCCCCGAGACCCTGAACCCATGGAAC   1536
TTCATGACTTTTGCTGGATCCATTTCCCTTAGTGGCTTCCAGAGCCCCAGTTGCAGGTCA   1596
AGTGAGGGCTGAGACAGCTAGAGTGGTCAAAAACTGCCATGGTGTTTTATGGGGGCAGTC   1656
CCAGGAAGTTGTTGCTCTTCCATGACCCCTCTGGATCTCCTGGGCTCTTGCCTGATTCTT   1716
GCTTCTGAGAGGCCCCAGTATTTTTTCCTTCTAAGGAGCTAACATCCTCTTCCATGAATA   1776
GCACAGCTCTTCAGCCTGAATGCTGACACTGCAGGGCGGTTCCAGCAAGTAGGAGCAAGT   1836
GGTGGCCTGGTAGGGCACAGAGGGCCCTTCAGGTTAGTGCTAAACTCTTAGGAAGTACCCT   1896
CTCCAAGCCCACCGAAATTCTTTTGATGCAAGAATCAGAGGCCCCATCAGGCAGAGTTGC   1956
TCTGTTATAGGATGGTAGGGCTGTAACTCAgTGGTCCAgTGTGCTTTTAGCATGCCCTGG   2016
GTTTGATCCTCAGCAACACATGCAAAACGTAAGTAGACAGCAGACAGCAGACAGCACAGC   2076
CAGCCCCCTGTGTGGTTTGCAGCCTCTGCCTTTGACTTTTACTCTGGTGGGCACACAGAG   2136
GGCTGGAGCTCCTCCTCCTGACCTTCCCAGGCCCCTGCAGCCACCTGTCTCTTCCTACCTCA   2196
GGAATGTCAGGGACTGTAGAGTTCCCCAACGgCTTGGTACTGTACTTGCTGTGACCCCAAC   2256
GCCTGGAGCACTCCCTCTAACTCCCCAACGGCTTGGTACTGTACTTGCTGTGACCCCAAC   2316
GTGCATTGTCCGGGTTAGGCACTGTGAGTTGGAACAGCTCATGACATCGGTTGAAAGGCC   2376
CACCCGGAAACAGCTAAGCCAGCTCTTTTGCCAAAGGATTCATGCCGGTTTTCTAATCAa   2436
CCTGCTCCCTAGCATTGCCTGGAAGGAAAGGGTTCAGGAGACTCCTCAAGAAGCAAGTTC   2496
AGTCTCAGGTGCTTGGATGCCATGCTCACCGATTCCACTGGATATGAACTTGGCAGAGGA   2556
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Figure 3C

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GCCTAGTTGTTGCCATGGAGACTTAAAGAGCTCAGCACTCTGGAATCAAGATACTGGACA   2616
CTTGGGGCCGACTTGTTAAGGCTCTGCAGCATCAGACTGTAGAGGGGAAGGAACACGTCT   2676
GCCCCCTGGTGGCCCGTCCTGGGAtGACCTCGGGCCtCCTAGGCAACAAAAGAATGAATT   2736
GGAAAGGATGTTCCTGGGTGTGGCCTAGCTCCTGTGCTTGTGTGGATCCCTAAAGGGTGT   2796
GCTAAGGAGCAATTGCACTGTGTGCTGGACAGAATTCCTGCTTATAAATGCTTTTTGTTG   2856
TTGTTTTGTACACTGAGCCCTGGCTGAGCCACCCCACCCCACCTCCCATCCCACCTTTAC   2916
ACGCCACTCTTGCATGAGAACCTGGCTGTCTCCCACTTGTAGCCTGTGGATGCTGAGGAA   2976
ACACCCAGCCAAGTAGACTCCAGGCTTgCCCCTATCTCCTGcTaTGAGTcTggCCTCCTC   3036
AtTgTGTTGTGGGAAgGAGACGGGtTCTGTCATCTCGGAAcgCCCACACCGTGGATGTGA   3096
ACAaTGGCTGTACTAGCTTAGACCAgCTTAGGGCTCTGCATATCACAGGAGGGGGAGCAG   3156
GGAACAATTTGAGTGCTGACCTATAACACAgTTCCTAAAGGATCGGGCAGTCCAGAATCT   3216
CCTCCTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCCATGTT       3276
TGCATGTATGTGTGTGCCAGTGTGTGGAGGCCCGAGGTTGGCTTTGGGTGTGTTTGATCA   3336
CTCTCCAGTTACTGAGGCGGGCTCTCATCTGTACCCAGAGCTTGCACATTTTCTAGTCTA   3396
ACTTGATTCAGGGATCTCTGTCTGCCTATGGAGgTGCTCAGGTTACAGGCAGGCTGCCAT   3456
ACCTGCCCGACATTTACATGAATACTAGAGATCTGAATTCTGGTCCTCACACTTGTATAC   3516
CTGCATTTTATCCACTAAGACATCTCTCCAAGGGCTCCCCCTTCCTATTTAATAAGTTAG   3576
TTTTGAACTGGCAAGATGGCTCAGTGGGTAAGGCAGTTTGCGGACAAACCTGATGACCTG   3636
AGTTGGATCCCTGACCATAAGGTAGAAGAGACCTGATTCCTGCAAGTTGTCCTCTGACCA   3696
CCACCCCATACATGCTTCTGCATATGTGCACACATCACATTCTTGCACACACACTCACAT   3756
ACCATAAATGTAATAAATTTTTTTAAATAAATTGATTTTATCTTTTAAAAAAAAAAA      3813
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